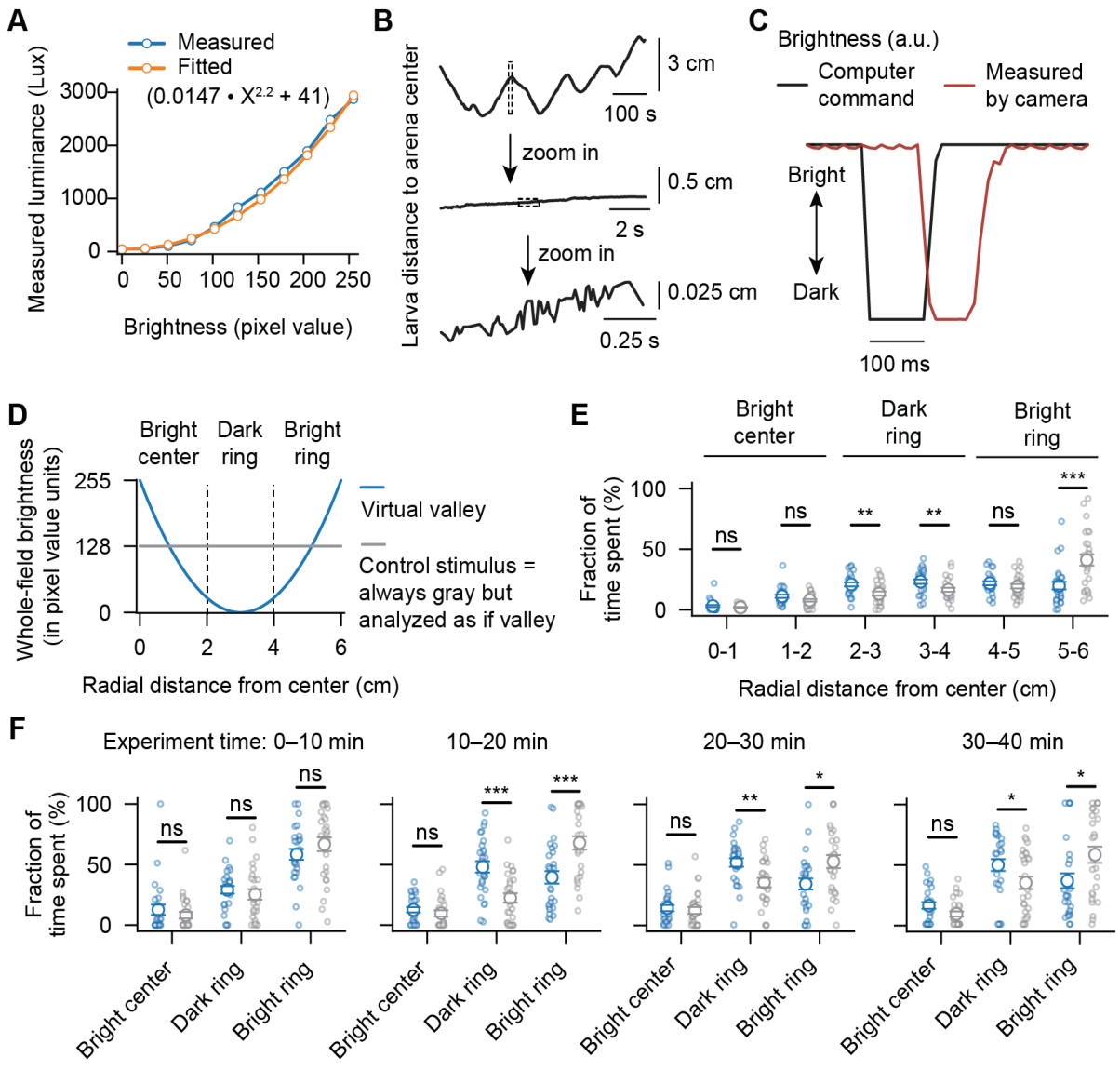


Figure S1. Performance of the closed-loop behavior setup and detailed behavior quantification. (**A**) Luminance as a function of computer pixel brightness, measured with a professional light meter and fitting results. As it is unclear how the larval visual system processes contrast, we did not attempt to linearize this curve. (**B**) Example raw tracking data, displayed in form of the radial distance to the center of the arena. Changes in the slope of this curve indicate events where the larva makes a turn. When zooming into this trace, it becomes visible that tracking noise is very small, in the order of ±0.025 cm (within a period of 0.25 s). Given our position-dependent brightness function (**Fig. 1B**), this would lead to a maximum pixel brightness fluctuation of as small as ±3 over the same short time period. (**C**) Measurement of the closed-loop delay of the system: We remove the infrared filters from the camera and directly measure the luminance coming from the projector. The projector starts with a high level of brightness. After a few seconds, it rapidly switches to a dark state. Whenever the camera detects this event, we automatically set

the brightness level back to a bright state again. The time of darkness is the full closed-loop delay of the system. **(D)** Luminance profile used for the "Valley" stimulus (same panel as in **Fig. 1B**). (**E**) Fraction of time larvae spend in the different regions for finer radial bin size (left to right: $p = 0.264$, $p = 0.060$, $p = 0.002$, $p = 0.009$, $p = 0.310$, $p < 0.001$; two-sided t-tests). (**F**) Fraction of time spent in the different regions, analyzed in 10 min time bins (left to right: $p = 0.360$, $p = 0.481$, $p = 0.256$ for first period; $p = 0.053$, $p < 0.001$, $p < 0.001$ for second period; $p = 0.616$, $p = 0.002$, $p = 0.011$ for third period; $p = 0.054$, $p = 0.044$, $p = 0.022$ for third period; two-sided t-tests). Error bars represent mean ± SEM. Blue dots indicate "Valley" stimulus larvae. Gray dots indicate "Constant" stimulus larvae. N = 27 larvae for both groups. Open circles represent individual animals.

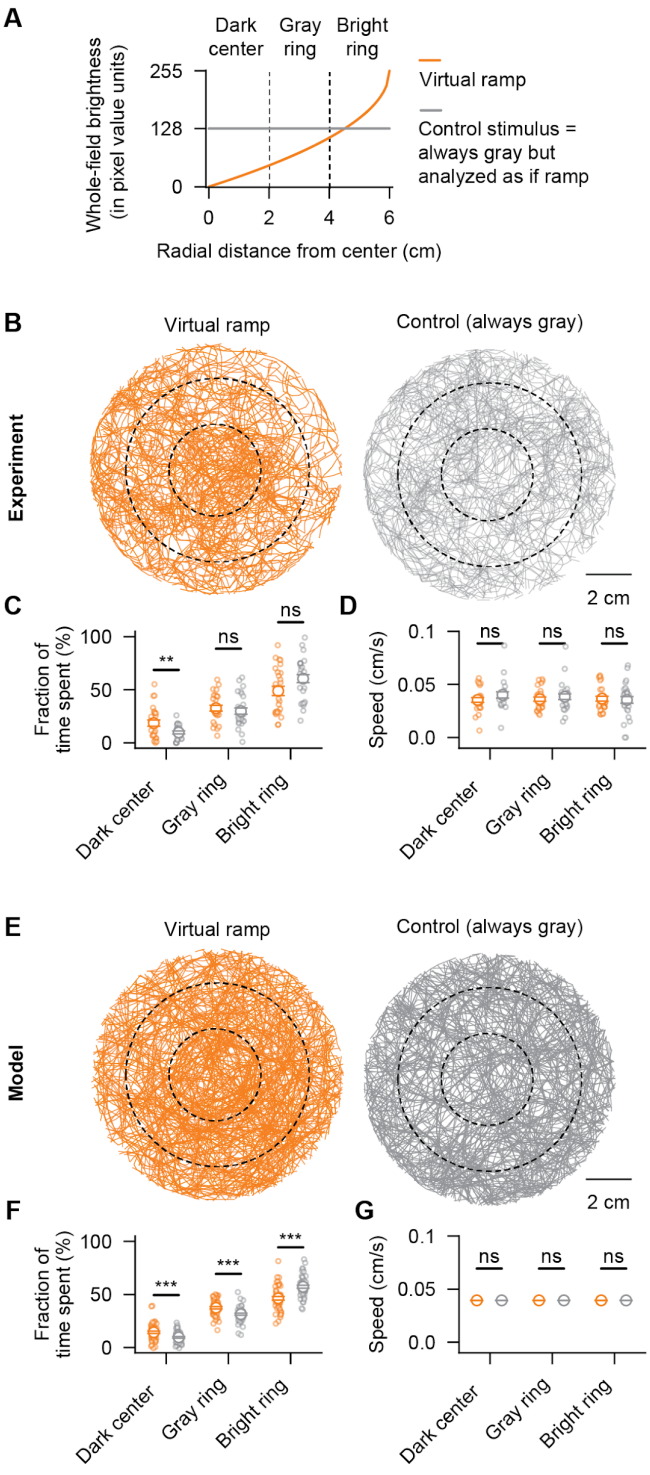


Figure S2. Temporal phototaxis in the alternative "Ramp" stimulus configuration (experimental data and modeling). (**A**) Whole-field brightness as a function of larval position for the "Ramp" stimulus and the "Control" stimulus. (**B**) Raw trajectories. Dashed circles delineate the "Dark" center, the "Gray" ring, and the "Bright" ring. (**C**) Fraction of time spent in each region (left to right: $p = 0.009$, $p = 0.484$, $p = 0.051$; two-sided t-tests). (**D**) Crawling speed in each region (left to right: $p = 0.200$ $p = 0.479$, $p = 0.770$; two-sided t-tests). N = 26 and N = 27 larvae for the "Ramp" stimulus and the "Constant" stimulus, respectively. Open circles represent individual animals. (**E–G**) Same as in (**B–D**) but for model simulations. (**F,G**) left to right: $p < 0.001$, $p < 0.001$, $p < 0.001$ in (**F**) and $p = 0.296$, $p = 0.677$, $p = 0.213$ in (**G**). N = 50 simulated larvae in both groups in **E–G**. Model parameters are the same as used in **Fig. 3B–I**. Error bars represent mean ± SEM. Orange dots and lines indicate "Ramp" stimulus larvae; Gray dots and lines indicate "Constant" stimulus larvae.

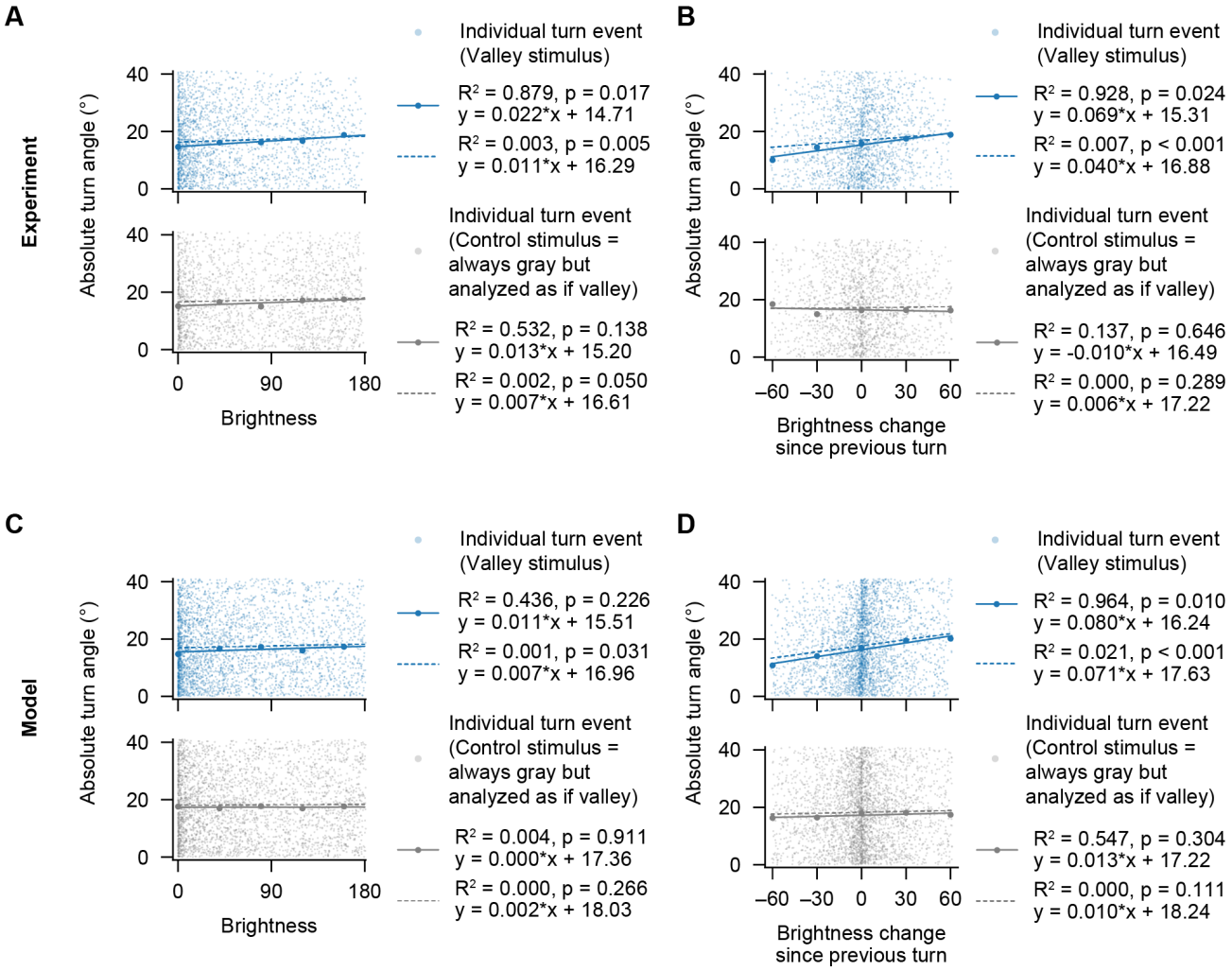
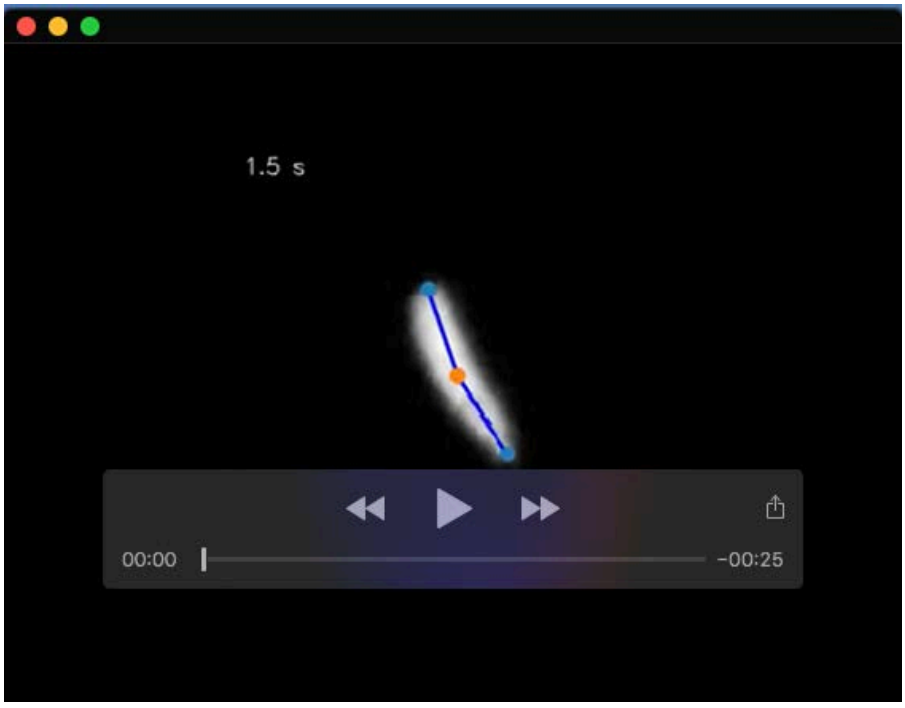


Figure S3. Regression analysis on individual turn events (experimental data and modeling). (A,B) Absolute turn angle as a function of instantaneous brightness (**A**) and as a function of brightness change since the previous turn (**B**) for "Valley" stimulus larvae (blue) and "Constant" stimulus larvae (gray). Small dots represent individual turns (n = 3153 and n = 2981 events, respectively, from N = 27 larvae for each group). Bigger filled dots are binned data. Regression analysis was performed on binned data (solid lines) as well as on raw data points (dashed lines). (**C,D**) Same analysis as in (**A,B**) but for model simulations. P values are based on a bootstrapping approach by repeating the regression analysis 1000 times for shuffled raw data and then comparing the distribution of R^2 values to the one from the original dataset.

Movie 1



Movie 2